CLAIMS

We claim:

1. A composition comprising:
    a) a first nucleic acid comprising a first ETM with a first redox potential; and
    b) a second nucleic acid comprising a second ETM with a second redox potential, wherein said first and said second redox potentials are different.

2. A composition according to claim 1 wherein the sequences of said first and said second nucleic acids are different.

3. A composition according to claim 2 wherein the sequence of said first and said second nucleic acids differ by only one base.

4. A composition according to claim 1 wherein said nucleic acids are single stranded.

5. A composition according to claim 1 further comprising:
    a) a third nucleic acid comprising a third ETM with a third redox potential; and
    b) a fourth nucleic acid comprising a fourth ETM with a fourth redox potential, wherein said first, second, third and fourth redox potentials are different.

6. A composition according to claim 5 wherein said first, second, third and fourth nucleic acids differ by only one base.

7. A composition according to claim 1 wherein said first and second ETMs are ferrocene derivatives.

8. A composition comprising:
    a) a substrate with a plurality of array locations, each array location comprising a covalently attached capture probe; and
    b) a plurality of competimers, wherein each competimer hybridizes to either:
        i) a capture probe;
        ii) a first portion of a capture extender probe, wherein said capture extender probe, if present, comprises a first portion that hybridizes to a domain of a target sequence and a second portion that hybridizes to said capture probe; or
        iii) a first portion of a label probe, wherein said label probe, if present, comprises a first portion that hybridizes to a domain of a target sequence and a second portion that comprises at least one electron transfer moiety (ETM).

9. A composition according to claim 8 wherein each competimer is perfectly complementary to said

capture probe or said first portion.

10. A composition according to claim 8, wherein said each array location is an electrode.

11. A composition according to claim 9, wherein each electrode further comprises a SAM.

12. A method of generating a hybridization kinetics curve in an assay for the presence of a target sequence in a sample comprising:

a) contacting said sample with an array comprising a plurality of capture probes, such that said target sequence binds to at least one of said capture probes to form a hybridization complex, wherein said hybridization complex comprises a label;

b) measuring the presence of said target sequence at least two times;

wherein said method does not remove labels that are not part of said hybridization complex between each measurement.

13. A method according to claim 12 wherein at least two of said measurements are done at different temperatures.

14. A method of detecting the presence of a target sequence in a sample comprising:

a) providing an array comprising a plurality of capture probes covalently attached to a solid support;

b) contacting said array with said sample under conditions wherein at least one assay complex comprising a target sequence, a capture probe and a detectable label is formed;

c) contacting said array with a plurality of competimers; and

d) detecting the presence or absence of said detectable label as an indication of the presence or absence of said target sequence.

15. A method according to claim 14 wherein said competimers are added with said sample.

16. A method according to claim 14 wherein said competimers are added after the formation of said assay complex.

17. A method according to claim 14 wherein said solid support is an electrode and said detectable label is an ETM.

18. A method for detecting the presence of a target sequence comprising:

a) providing an assay complex comprising a target sequence and a capture probe covalently attached to an electrode, wherein said assay complex comprises at least one ETM;

b) detecting the presence or absence of said ETM at at least two different times.

19. A method according to claim 18 wherein said detecting is done at at least two different temperatures.

20. A method according to claim 18 wherein said ETM is covalently attached to said target sequence.

21. A method according to claim 18 wherein said ETM is covalently attached to a label probe that hybridizes to a label domain of said target sequence.

22. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a hybridization complex comprising said target sequence and a capture probe covalently attached to an electrode; and

b) determining the nucleotide at said detection position.

23. A method according to claim 22 wherein said determining comprises:

a) contacting said array with a plurality of detection probes each comprising:

i) a unique nucleotide at the interrogation position; and

ii) an ETM with a unique redox potential; and

b) detecting a signal from at least one of said ETMs to identify the nucleotide at the detection position.

24. A method according to claim 22 wherein said target sequence comprises a first target domain directly 5' adjacent to said detection position, wherein said hybridization complex comprises said target sequence, said capture probe and an extension primer hybridized to said first target domain of said target sequence, and said determining comprises:

a) contacting said array with:

i) a polymerase enzyme; and

ii) a plurality of NTPs each comprising a covalently attached ETM;

under conditions whereby if one of said NTPs basepairs with the base at said detection position, said extension primer is extended by said enzyme to incorporate said ETM; and

b) identifying the base at said detection position.

25. A method according to claim 24 wherein each NTP comprises an ETM with a different redox potential.

26. A method according to claim 22 wherein said target sequence comprises a first target domain directly 5' adjacent to said detection position, wherein said capture proves serves an an extension primer and is hybridized to said first target domain, and said determining comprises:

a) contacting said array with:

i) a polymerase enzyme; and

ii) a plurality of NTPs each comprising a covalently attached ETM;

under conditions whereby if one of said NTPs basepairs with the base at said detection position, said capture probe is extended by said enzyme to incorporate said ETM; and

b) identifying the base at said detection position.

27. A method according to claim 22 wherein said target sequence comprises 5' to 3':

a) a first target domain comprising an overlap domain comprising at least a nucleotide in the detection position; and

b) a second target domain contiguous with said detection position;

said method comprising:

a) hybridizing a first probe to said first target domain; and

b) hybridizing a second probe to said second target domain, wherein said second probe comprises a detection sequence that does not hybridize with said target sequence;

wherein if said second probe comprises a base that is perfectly complementary to said detection position a cleavage structure is formed;

c) providing a cleavage enzyme that will cleave said detection sequence;

d) forming an assay complex with said detection sequence, a capture probe covalently attached to an electrode, and at least one ETM;

e) detecting the presence or absence of said ETM as an indication of the formation of said cleavage structure; and

f) identifying the base at said detection position.

28. A method according to claim 24 wherein said detection sequence comprises at least one ETM.

29. A method according to claim 22 wherein said target sequence comprises a first target domain comprising said detection position and a second target domain adjacent to said detection position, said method comprising:

a) hybridizing a first ligation probe to said first target domain;

b) hybridizing a second ligation probe to said second target domain, wherein if said second ligation probe comprises a base that is perfectly complementary to said detection position a ligation structure is formed;

c) providing a ligation enzyme that will ligate said first and said second ligation probes to form a ligated probe;

d) forming an assay complex with said ligated probe, a capture probe covalently attached to an electrode, and at least one ETM;

e) detecting the presence or absence of said ETM as an indication of the formation of said

ligation structure; and

f) identifying the base at said detection position.

30. A method according to claim 29 wherein said first ligation probe comprises said ETM and said capture probe will hybridize to said second ligation probe or a a first portion of a capture extender probe, wherein said capture extender probe, if present, comprises a first portion that hybridizes to said capture probe and a second portion that hybridizes to said second ligation probe.

31. A method according to claim 29 wherein said first ligation probe comprises a portion that will hybridize to a label probe comprising at least one ETM.

32. A surface comprising a self-assembled monolayer (SAM), wherein said SAM comprises at least one photocleavable species.

33. A surface according to claim 32 wherein said surface is gold.

34. A surface comprising a SAM comprising:

a) a first species comprising insulators; and

b) a second species comprising a electroconduit forming species (EFS), wherein said EFS is not a conductive oligomer.

35. A surface according to claim 33 or 34 wherein said SAM comprises a species comprising a target analyte.

36. A surface according to claim 35 wherein said target analyte is a nucleic acid.

37. A method of detecting the presence of a target analyte in a sample comprising:

a) adding said target analyte to an electrode comprising:

i) a first SAM forming species comprising a capture binding ligand; and

ii) at least a second SAM forming species;

b) forming a hybridization complex comprising said target analyte and said capture binding ligand;

c) adding a third SAM forming species that replaces said second SAM forming species;

d) forming an assay complex comprising said target analyte, said capture binding ligand, and at least one electron transfer moiety (ETM); and

e) detecting the presence or absence of said ETM as an indication of the presence or absence of said target analyte.

38. A method of detecting a target analyte in a sample comprising:

a) binding a target analyte to an electrode comprising a covalently attached capture binding ligand;

b) binding a solution binding ligand to said target analyte, wherein said solution binding ligand comprises a first portion that will bind to a target analyte and a directly or indirectly attached recruitment linker comprising a first portion comprising at least one conductive oligomer comprising at least one ETM; and

d) detecting the presence of said ETM using said electrode as an indication of the presence of the target analyte.

39. A method of adding at least one ETM to a nucleic acid, said method comprising:

a) providing a nucleic acid comprising a first functional group;

b) providing at least one ETM with a second functional group; and

c) joining said first and said second functional groups to form a covalent attachment.

40. A method according to claim 39 wherein said nucleic acid comprises a ribose-phosphate backbone and said first functional group is at the 2' position of said ribose.

41. A method according to claim 39 wherein said first functional group comprises an amine.

42. A method according to claim 39 wherein said first functional group is attached to a base of said nucleic acid.